

=> d his full

(FILE 'HOME' ENTERED AT 17:33:10 ON 11 APR 2007)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007  
SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

31 FILE ADISCTI  
10 FILE ADISINSIGHT  
27 FILE ADISNEWS  
3911 FILE AGRICOLA  
116 FILE ANABSTR  
16 FILE ANTE  
41 FILE AQUALINE  
1216 FILE AQUASCI  
3267 FILE BIOENG  
30282 FILE BIOSIS  
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4 FILE CROPB  
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29 FILE DDFB  
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515097 FILE GENBANK  
61 FILE HEALSAFE  
6488 FILE IFIPAT  
12 FILE IMSDRUGNEWS  
9 FILE IMSRESEARCH  
25 FILE KOSMET  
17980 FILE LIFESCI  
39232 FILE MEDLINE  
240 FILE NTIS  
1 FILE NUTRACEUT  
371 FILE OCEAN  
13245 FILE PASCAL  
1 FILE PHAR  
6 FILE PHARMAML  
84 FILE PHIN  
745 FILE PROMT  
3 FILE PROUSDDR  
3 FILE RDISCLOSURE  
19895 FILE SCISEARCH  
9853 FILE TOXCENTER  
65679 FILE USPATFULL  
7383 FILE USPAT2  
1 FILE VETB  
161 FILE VETU  
68 FILE WATER  
8559 FILE WPIDS

31 FILE WPIFV  
8559 FILE WPINDEX  
42 FILE IPA  
4 FILE NAPRALERT  
555 FILE NLDB

L1      QUE RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

-----  
D RANK

FILE 'GENBANK, USPATFULL, MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH,  
BIOTECHNO, LIFESCI, PASCAL, CABA' ENTERED AT 17:37:30 ON 11 APR 2007

L2      790629 SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

L3      739 SEA L2(S) PYLORI?

L4      49 SEA L3 AND (BCC? OR ?CCATC?)

L5      47 DUP REM L4 (2 DUPLICATES REMOVED)

        D TI L5 1-45

        D TI L5 46-47

L6      31 SEA L3 AND (BCC? OR CCATC?)

L7      29 DUP REM L6 (2 DUPLICATES REMOVED)

        D L7 1-29

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1652dmr

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America  
NEWS 2 "Ask CAS" for self-help around the clock  
NEWS 3 DEC 18 CA/CAPLUS pre-1967 chemical substance index entries enhanced  
with preparation role  
NEWS 4 DEC 18 CA/CAPLUS patent kind codes updated  
NEWS 5 DEC 18 MARPAT to CA/CAPLUS accession number crossover limit increased  
to 50,000  
NEWS 6 DEC 18 MEDLINE updated in preparation for 2007 reload  
NEWS 7 DEC 27 CA/CAPLUS enhanced with more pre-1907 records  
NEWS 8 JAN 08 CHEMLIST enhanced with New Zealand Inventory of Chemicals  
NEWS 9 JAN 16 CA/CAPLUS Company Name Thesaurus enhanced and reloaded  
NEWS 10 JAN 16 IPC version 2007.01 thesaurus available on STN  
NEWS 11 JAN 16 WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data  
NEWS 12 JAN 22 CA/CAPLUS updated with revised CAS roles  
NEWS 13 JAN 22 CA/CAPLUS enhanced with patent applications from India  
NEWS 14 JAN 29 PHAR reloaded with new search and display fields  
NEWS 15 JAN 29 CAS Registry Number crossover limit increased to 300,000 in  
multiple databases  
NEWS 16 FEB 15 PATDPASPC enhanced with Drug Approval numbers  
NEWS 17 FEB 15 RUSSIAPAT enhanced with pre-1994 records  
NEWS 18 FEB 23 KOREAPAT enhanced with IPC 8 features and functionality  
NEWS 19 FEB 26 MEDLINE reloaded with enhancements  
NEWS 20 FEB 26 EMBASE enhanced with Clinical Trial Number field  
NEWS 21 FEB 26 TOXCENTER enhanced with reloaded MEDLINE  
NEWS 22 FEB 26 IFICDB/IFIPAT/IFIUDB reloaded with enhancements  
NEWS 23 FEB 26 CAS Registry Number crossover limit increased from 10,000  
to 300,000 in multiple databases  
NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display format  
NEWS 25 MAR 16 CASREACT coverage extended  
NEWS 26 MAR 20 MARPAT now updated daily  
NEWS 27 MAR 22 LWPI reloaded  
NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements  
NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN  
NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN  
  
NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT  
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),  
AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.  
  
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NEWS X25 X.25 communication option no longer available

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FILE 'HOME' ENTERED AT 17:33:10 ON 11 APR 2007

=> index bioscience medicine

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE

ENTRY TOTAL

SESSION

FULL ESTIMATED COST

0.21

0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=>

=> s restricti? (s) (enzym? or endonucleas?)

31 FILE ADISCTI  
10 FILE ADISINSIGHT  
27 FILE ADISNEWS  
3911 FILE AGRICOLA  
116 FILE ANABSTR  
16 FILE ANTE  
41 FILE AQUALINE  
1216 FILE AQUASCI  
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19601 FILE BIOTECHNO  
10704 FILE CABA  
37645 FILE CAPLUS  
790 FILE CEABA-VTB  
81 FILE CIN  
319 FILE CONFSCI  
4 FILE CROPB  
133 FILE CROPU  
29 FILE DDFB

21 FILES SEARCHED...

170 FILE DDFU  
38469 FILE DGENE  
2384 FILE DISSABS  
29 FILE DRUGB  
566 FILE DRUGU  
125 FILE EMBAL  
21269 FILE EMBASE  
10560 FILE ESBIODBASE  
16 FILE FOREGE  
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6488 FILE IFIPAT  
12 FILE IMSDRUGNEWS  
9 FILE IMSRESEARCH  
25 FILE KOSMET

17980 FILE LIFESCI  
 42 FILES SEARCHED...  
 39232 FILE MEDLINE  
 240 FILE NTIS  
 1 FILE NUTRACEUT  
 371 FILE OCEAN  
 13245 FILE PASCAL  
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 84 FILE PHIN  
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 3 FILE RDISCLOSURE  
 19895 FILE SCISEARCH  
 9853 FILE TOXCENTER  
 65679 FILE USPATFULL  
 7383 FILE USPAT2  
 1 FILE VETB  
 161 FILE VETU  
 68 FILE WATER  
 8559 FILE WPIDS  
 65 FILES SEARCHED...  
 31 FILE WPIFV  
 8559 FILE WPINDEX  
 42 FILE IPA  
 4 FILE NAPRALERT  
 555 FILE NLDB

63 FILES HAVE ONE OR MORE ANSWERS, 70 FILES SEARCHED IN STNINDEX

L1 QUE RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

=> d rank

F1	515097	GENBANK
F2	65679	USPATFULL
F3	39232	MEDLINE
F4	38469	DGENE
F5	37645	CAPLUS
F6	30282	BIOSIS
F7	21269	EMBASE
F8	19895	SCISEARCH
F9	19601	BIOTECHNO
F10	17980	LIFESCI
F11	13245	PASCAL
F12	10704	CABA
F13	10641	BIOTECHABS
F14	10641	BIOTECHDS
F15	10560	ESBIOBASE
F16	9853	TOXCENTER
F17	8559	WPIDS
F18	8559	WPINDEX
F19	7383	USPAT2
F20	6488	IFIPAT
F21	3911	AGRICOLA
F22	3267	BIOENG
F23	2384	DISSABS
F24	1216	AQUASCI
F25	1211	FSTA
F26	790	CEABA-VTB
F27	745	PROMT
F28	566	DRUGU
F29	555	NLDB
F30	411	FROSTI
F31	371	OCEAN
F32	319	CONFSCI

F33	240	NTIS
F34	170	DDFU
F35	161	VETU
F36	133	CROPU
F37	125	EMBAL
F38	116	ANABSTR
F39	84	PHIN
F40	81	CIN
F41	68	WATER
F42	61	HEALSAFE
F43	42	IPA
F44	41	AQUALINE
F45	31	ADISCTI
F46	31	WPIFV
F47	29	DDFB
F48	29	DRUGB
F49	27	ADISNEWS
F50	25	KOSMET
F51	16	ANTE
F52	16	FOREGE
F53	12	IMSDRUGNEWS
F54	10	ADISINSIGHT
F55	9	IMSRESEARCH
F56	6	PHARMAML
F57	4	CROPB
F58	4	NAPRALERT
F59	3	PROUSDDR
F60	3	RDISCLOSURE
F61	1	NUTRACEUT
F62	1	PHAR
F63	1	VETB

=> file f1-f3, f5-12

COST IN U.S. DOLLARS

SINCE FILE  
ENTRY

TOTAL  
SESSION

FULL ESTIMATED COST

3.78

3.99

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FILE 'USPATFULL' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'MEDLINE' ENTERED AT 17:37:30 ON 11 APR 2007

FILE 'CAPLUS' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'LIFESCI' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'CABA' ENTERED AT 17:37:30 ON 11 APR 2007  
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=> s restricti? (s) (enzym? or endonucleas?)  
L2 790629 RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

=> s l2(s) pylori?  
L3 739 L2(S) PYLORI?

=> s l3 and (bcc? or ?ccatc?)  
2 FILES SEARCHED...

LEFT TRUNCATION IGNORED FOR FILE 'LIFESCI'

L4 49 L3 AND (BCC? OR ?CCATC?)

Left truncation is not valid in the specified search field in the  
specified file. The term has been searched without left truncation.  
Examples: '?TERPEN?' would be searched as 'TERPEN?' and '?FLAVONOID'  
would be searched as 'FLAVONOID.'

If you are searching in a field that uses implied proximity, and you  
used a truncation symbol after a punctuation mark, the system may  
interpret the truncation symbol as being at the beginning of a term.  
Implied proximity is used in search fields indexed as single words,  
for example, the Basic Index.

=> dup rem l4  
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.  
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE  
PROCESSING COMPLETED FOR L4  
L5 47 DUP REM L4 (2 DUPLICATES REMOVED)

=> d ti l5 1-45

L5 ANSWER 1 OF 47 USPATFULL on STN DUPLICATE 1  
TI Type II restriction endonuclease and application thereof

L5 ANSWER 2 OF 47 USPATFULL on STN  
TI Genes of an otitis media isolate of haemophilus influenzae

L5 ANSWER 3 OF 47 USPATFULL on STN  
TI H. pylori fucosyltransferases

L5 ANSWER 4 OF 47 USPATFULL on STN  
TI Microorganisms and assays for the identification of antibiotics

L5 ANSWER 5 OF 47 USPATFULL on STN  
TI Computer based versatile method for identifying protein coding DNA  
sequences useful as drug targets

L5 ANSWER 6 OF 47 USPATFULL on STN  
TI Methods for high throughput genome analysis using restriction site  
tagged microarrays

L5 ANSWER 7 OF 47 USPATFULL on STN  
TI Proteins, in particular membrane proteins, of Helicobacter pylori, their  
preparation and use

L5 ANSWER 8 OF 47 USPATFULL on STN  
TI Nucleic acid and amino acid sequences relating to Helicobacter pylori

for diagnostics and therapeutics

- L5 ANSWER 9 OF 47 USPATFULL on STN  
TI Plasmid DNA from *Yersinia pestis*
- L5 ANSWER 10 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2  
TI Isolation and Characterization of a HpyC1I Restriction-Modification System in *Helicobacter pylori*
- L5 ANSWER 11 OF 47 USPATFULL on STN  
TI dapE gene of *Helicobacter pylori* and dapE- mutant strains of *Helicobacter pylori*
- L5 ANSWER 12 OF 47 USPATFULL on STN  
TI *Helicobacter pylori* antigen
- L5 ANSWER 13 OF 47 USPATFULL on STN  
TI dapE gene on *Helicobacter pylori* and dapE- mutant strains of *Helicobacter pylori*
- L5 ANSWER 14 OF 47 USPATFULL on STN  
TI Nucleotide sequence of the *Mycoplasma genitalium* genome, fragments thereof, and uses thereof
- L5 ANSWER 15 OF 47 USPATFULL on STN  
TI Bacterial antigens and vaccine compositions
- L5 ANSWER 16 OF 47 USPATFULL on STN  
TI Microorganisms and assays for the identification of antibiotics
- L5 ANSWER 17 OF 47 USPATFULL on STN  
TI DNA adenine methyltransferases and uses thereof
- L5 ANSWER 18 OF 47 USPATFULL on STN  
TI RECOMBINANT MICROORGANISMS EXPRESSING ANTIGENIC PROTEINS OF *HELICOBACTER PYLORI*
- L5 ANSWER 19 OF 47 USPATFULL on STN  
TI Compositions and methods relating to drug discovery and detection and treatment of gastrointestinal diseases
- L5 ANSWER 20 OF 47 USPATFULL on STN  
TI Bacterial antigens and vaccine compositions
- L5 ANSWER 21 OF 47 USPATFULL on STN  
TI Compositions comprising isolated *Helicobacter pylori* CagI polynucleotides and method of preparation thereof
- L5 ANSWER 22 OF 47 USPATFULL on STN  
TI *Helicobacter* TagA gene fusion protein
- L5 ANSWER 23 OF 47 USPATFULL on STN  
TI Purified vacuolating toxin from *Helicobacter pylori* and methods to use same
- L5 ANSWER 24 OF 47 USPATFULL on STN  
TI Immunogenic compositions against *Helicobacter* infection, polypeptides for use in the compositions, and nucleic acid sequences encoding said polypeptides
- L5 ANSWER 25 OF 47 USPATFULL on STN  
TI Nucleotide sequences coding for a protein with urease activity
- L5 ANSWER 26 OF 47 USPATFULL on STN  
TI Vacuolating toxin-deficient *H. pylori*



L5 ANSWER 27 OF 47 USPATFULL on STN  
 TI Taga gene and methods for detecting predisposition to peptic ulceration

L5 ANSWER 28 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): The complete genome sequence of the European  
 Francisella tularensis subspecies tularensis isolate  
 FSC 198 suggests that it is derived from the archetypal  
 laboratory strain Schu S4, originally isolated in North  
 America  
 TITLE (TI): Direct Submission

L5 ANSWER 29 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): Who ate whom? Adaptive Helicobacter genomic changes  
 that accompanied a host jump from early humans to large  
 felines  
 TITLE (TI): Direct Submission

L5 ANSWER 30 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): Extensive DNA inversions in the B. fragilis genome  
 control variable gene expression  
 TITLE (TI): Direct Submission

L5 ANSWER 31 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): The Complete Genome Sequence of Neisseria gonorrhoeae  
 TITLE (TI): Direct Submission

L5 ANSWER 32 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): The complete genome sequence of Francisella tularensis,  
 the causative agent of tularemia  
 TITLE (TI): Direct Submission

L5 ANSWER 33 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): Genome sequence of Streptococcus mutans UA159, a  
 cariogenic dental pathogen  
 TITLE (TI): Direct Submission

L5 ANSWER 34 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): Genome Sequence of Yersinia pestis KIM  
 TITLE (TI): Direct Submission

L5 ANSWER 35 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): The genome sequence of the food-borne pathogen  
 Campylobacter jejuni reveals hypervariable sequences  
 TITLE (TI): Re-annotation of Campylobacter jejuni NCTC11168  
 TITLE (TI): Direct Submission  
 TITLE (TI): Direct Submission

L5 ANSWER 36 OF 47 GENBANK® COPYRIGHT 2007 on STN  
 TITLE (TI): Complete nucleotide sequence of the prophage VT2-Sakai  
 carrying the verotoxin 2 genes of the enterohemorrhagic  
 Escherichia coli O157:H7 derived from the Sakai  
 outbreak  
 TITLE (TI): Comparative analysis of the whole set of rRNA operons  
 between an enterohemorrhagic Escherichia coli O157:H7  
 Sakai strain and an Escherichia coli K-12 strain MG1655

TITLE (TI): Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic *Escherichia coli* O157:H7 strain derived from the Sakai outbreak

TITLE (TI): Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12

TITLE (TI): Direct Submission

L5 ANSWER 37 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*

TITLE (TI): Direct Submission

L5 ANSWER 38 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Insights into the evolution of *Yersinia pestis* through whole-genome comparison with *Yersinia pseudotuberculosis*

TITLE (TI): Direct Submission

L5 ANSWER 39 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): The genome sequence of the enterobacterial phytopathogen *Erwinia carotovora* subsp. *atroseptica* SCRI1043 and functional genomic identification of novel virulence factors

TITLE (TI): Direct Submission

L5 ANSWER 40 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance

TITLE (TI): Direct Submission

L5 ANSWER 41 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance

TITLE (TI): Direct Submission

L5 ANSWER 42 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genome sequence of an M1 strain of *Streptococcus pyogenes*

TITLE (TI): Direct Submission

L5 ANSWER 43 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7

TITLE (TI): Direct Submission

L5 ANSWER 44 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

TITLE (TI): Direct Submission

L5 ANSWER 45 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of

TITLE (TI): Neisseria meningitidis Z2491  
Direct Submission

=> d ti 15 46-47

L5 ANSWER 46 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of  
Neisseria meningitidis Z2491  
TITLE (TI): Direct Submission

L5 ANSWER 47 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): The genome sequence of the food-borne pathogen  
Campylobacter jejuni reveals hypervariable sequences  
TITLE (TI): Direct Submission

=> s 13 and (bcc? or ccattc?)

L6 31 L3 AND (BCC? OR CCATC?)

=> dup rem 16

DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.

ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE

PROCESSING COMPLETED FOR L6

L7 29 DUP REM L6 (2 DUPLICATES REMOVED)

=> d 17 1-29

L7 ANSWER 1 OF 29 USPATFULL on STN DUPLICATE 1

AN 2005:233506 USPATFULL

TI Type II restriction endonuclease and application thereof

IN Wang, Jin-Town, Taipei, TAIWAN, PROVINCE OF CHINA

Lin, Tzu-Lung, Taipei, TAIWAN, PROVINCE OF CHINA

PI US 2005202443 A1 20050915

AI US 2004-796669 A1 20040309 (10)

DT Utility

FS APPLICATION

LN.CNT 612

INCL INCLM: 435/006.000

INCLS: 435/199.000; 435/252.300; 435/471.000; 536/023.200

NCL NCLM: 435/006.000

NCLS: 435/199.000; 435/252.300; 435/471.000; 536/023.200

IC [7]

ICM C12Q001-68

ICS C07H021-04; C12N009-10; C12N015-74

IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];

C12N0009-10 [ICS,7]; C12N0015-74 [ICS,7]

IPCR C07H0021-00 [I,C\*]; C07H0021-04 [I,A]; C12N0009-10 [I,C\*];

C12N0009-10 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];

C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 2 OF 29 USPATFULL on STN

AN 2005:189426 USPATFULL

TI H. pylori fucosyltransferases

IN Simala-Grant, Joanne, Edmonton, CANADA

Taylor, Diane, Edmonton, CANADA

Johnson, Karl F., Hatboro, PA, UNITED STATES

Bezila, Daniel James, Philadelphia, PA, UNITED STATES

PA Neose Technologies, Inc., Horsham, PA, UNITED STATES (non-U.S.  
corporation)

Governors of the University of Alberta, Edmonton, CANADA (non-U.S.  
corporation)

PI US 2005164338 A1 20050728  
 AI US 2004-764212 A1 20040122 (10)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 4386  
 INCL INCLM: 435/068.100  
 INCLS: 530/395.000; 435/193.000; 435/320.100; 435/325.000  
 NCL NCLM: 435/068.100  
 NCLS: 435/193.000; 435/320.100; 435/325.000; 530/395.000  
 IC [7]  
 ICM C12P021-06  
 ICS C12N009-10  
 IPCI C12P0021-06 [ICM,7]; C12N0009-10 [ICS,7]  
 IPCR C12N0009-10 [I,C\*]; C12N0009-10 [I,A]; C12P0021-06 [I,C\*];  
 C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 29 USPATFULL on STN  
 AN 2005:183455 USPATFULL  
 TI Microorganisms and assays for the identification of antibiotics  
 IN Yocum, R. Rogers, Lexington, MA, UNITED STATES  
 Patterson, Thomas A., North Attleboro, MA, UNITED STATES  
 PA OmniGene Bioproducts, Inc., Cambridge, MA, UNITED STATES, 02138 (U.S. corporation)  
 PI US 2005158842 A1 20050721  
 AI US 2004-11979 A1 20041213 (11)  
 RLI Division of Ser. No. US 2001-813453, filed on 20 Mar 2001, GRANTED, Pat. No. US 6830898  
 PRAI US 2000-227860P 20000824 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 4666  
 INCL INCLM: 435/252.300  
 INCLS: 435/471.000; 536/023.200  
 NCL NCLM: 435/252.300  
 NCLS: 435/471.000; 536/023.200  
 IC [7]  
 ICM C12N001-21  
 ICS C07H021-04; C12N015-74  
 IPCI C12N0001-21 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12N0015-74 [ICS,7]  
 IPCR C12N0009-12 [I,C\*]; C12N0009-12 [I,A]; C12N0015-52 [I,C\*];  
 C12N0015-52 [I,A]; C12N0015-54 [I,C\*]; C12N0015-54 [I,A];  
 C12P0013-00 [I,C\*]; C12P0013-02 [I,A]; C12P0017-02 [I,C\*];  
 C12P0017-04 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 29 USPATFULL on STN  
 AN 2005:158272 USPATFULL  
 TI Computer based versatile method for identifying protein coding DNA sequences useful as drug targets  
 IN Brahmachari, Samir Kumar, Delhi, INDIA  
 Dash, Debasis, Delhi, INDIA  
 Sharma, Ramakant, Delhi, INDIA  
 Maheshwari, Jitendra Kumar, Delhi, INDIA  
 PI US 2005136480 A1 20050623  
 AI US 2004-755415 A1 20040113 (10)  
 RLI Continuation-in-part of Ser. No. US 2003-727989, filed on 5 Dec 2003, PENDING  
 DT Utility  
 FS APPLICATION  
 LN.CNT 9116  
 INCL INCLM: 435/007.100  
 INCLS: 702/019.000  
 NCL NCLM: 435/007.100

NCLS: 702/019.000  
IC [7]  
ICM G01N033-53  
ICS G06F019-00; G01N033-48; G01N033-50  
IPCI G01N0033-53 [ICM,7]; G06F0019-00 [ICS,7]; G01N0033-48 [ICS,7];  
G01N0033-50 [ICS,7]  
IPCR G01N0033-48 [I,C\*]; G01N0033-48 [I,A]; G01N0033-50 [I,C\*];  
G01N0033-50 [I,A]; G01N0033-53 [I,C\*]; G01N0033-53 [I,A];  
G06F0019-00 [I,C\*]; G06F0019-00 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 29 USPATFULL on STN  
AN 2004:65910 USPATFULL  
TI Plasmid DNA from Yersinia pestis  
IN Blattner, Frederick R., Madison, WI, United States  
Burland, Valerie, Cross Plains, WI, United States  
Rose, Debra J., Fond du Lac, WI, United States  
Mayhew, George F., Madison, WI, United States  
Perna, Nicole, Madison, WI, United States  
Perry, Robert D, Lexington, KY, United States  
Straley, Susan C, Lexington, KY, United States  
Fetherston, Jacqueline D., Lexington, KY, United States  
Lindler, Luther E., Wheaton, MD, United States  
Plano, Gregory V., Miami, FL, United States  
PA Wisconsin Alumni Research Foundation, Madison, WI, United States (U.S.  
corporation)  
PI US 6706522 B1 20040316  
AI US 1999-409800 19990930 (9)  
DT Utility  
FS GRANTED  
LN.CNT 4492  
INCL INCLM: 435/320.100  
INCLS: 435/252.300; 536/023.100  
NCL NCLM: 435/320.100  
NCLS: 435/252.300; 536/023.100  
IC [7]  
ICM C12N015-63  
IPCI C12N0015-63 [ICM,7]  
IPCR C07K0014-195 [I,C\*]; C07K0014-24 [I,A]  
EXF 536/23.1; 435/320.1; 435/252.3  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 29 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2  
AN 2004:218217 CAPLUS  
DN 140:333344  
TI Isolation and Characterization of a HpyC1I Restriction-Modification System  
in Helicobacter pylori  
AU Lin, Tzu-Lung; Shun, Chia-Tun; Chang, Kai-Chih; Wang, Jin-Town  
CS College of Medicine, Graduate Institute of Microbiology, National Taiwan  
University, Taipei, 10016, Taiwan  
SO Journal of Biological Chemistry (2004), 279(12), 11156-11162  
CODEN: JBCHA3; ISSN: 0021-9258  
PB American Society for Biochemistry and Molecular Biology  
DT Journal  
LA English  
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 29 USPATFULL on STN  
AN 2003:81597 USPATFULL  
TI Nucleotide sequence of the mycoplasma genitalium genome, fragments  
thereof, and uses thereof  
IN Fraser, Claire M., Potomac, MD, United States  
Adams, Mark D., N. Potomac, MD, United States  
Gocayne, Jeannine D., Silver Spring, MD, United States

Hutchison, III, Clyde A., Chapel Hill, NC, United States  
 Smith, Hamilton O., Towson, MD, United States  
 Venter, J. Craig, Potomac, MD, United States  
 White, Owen, Gaithersburg, MD, United States  
 PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)  
 Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)  
 The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)  
 PI US 6537773 B1 20030325  
 AI US 1995-545528 19951019 (8)  
 RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, now abandoned  
 DT Utility  
 FS GRANTED  
 LN.CNT 15190  
 INCL INCLM: 435/069.100  
 INCLS: 536/023.700; 536/024.320; 435/252.300; 435/320.100  
 NCL NCLM: 435/069.100  
 NCLS: 435/252.300; 435/320.100; 536/023.700; 536/024.320  
 IC [7]  
 ICM C12Q001-68  
 IPCI C12Q0001-68 [ICM,7]  
 IPCR A61K0038-00 [N,C\*]; A61K0038-00 [N,A]; C07K0014-195 [I,C\*]; C07K0014-30 [I,A]  
 EXP 536/23.7; 536/23.1; 536/24.3; 536/24; 536/52; 435/69.1; 435/320.1  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 29 USPATFULL on STN  
 AN 2002:301138 USPATFULL  
 TI Microorganisms and assays for the identification of antibiotics  
 IN Yocum, R. Rogers, Lexington, MA, UNITED STATES  
 Patterson, Thomas A., North Attleboro, MA, UNITED STATES  
 PI US 2002168681 A1 20021114  
 US 6830898 B2 20041214  
 AI US 2001-813453 A1 20010320 (9)  
 PRAI US 2000-227860P 20000824 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 4858  
 INCL INCLM: 435/007.100  
 NCL NCLM: 435/032.000; 435/007.100  
 NCLS: 424/009.200; 435/007.100; 514/001.000; 530/300.000; 530/350.000  
 IC [7]  
 ICM G01N033-53  
 IPCI G01N0033-53 [ICM,7]  
 IPCI-2 C12Q0001-18 [ICM,7]; A01N0061-00 [ICS,7]; C07K0002-00 [ICS,7]; C07K0014-195 [ICS,7]; A61K0049-00 [ICS,7]  
 IPCR C12N0009-12 [I,C\*]; C12N0009-12 [I,A]; C12N0015-52 [I,C\*]; C12N0015-52 [I,A]; C12N0015-54 [I,C\*]; C12N0015-54 [I,A]; C12P0013-00 [I,C\*]; C12P0013-02 [I,A]; C12P0017-02 [I,C\*]; C12P0017-04 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 29 USPATFULL on STN  
 AN 2000:57536 USPATFULL  
 TI Compositions and methods relating to drug discovery and detection and treatment of gastrointestinal diseases  
 IN Corthesy-Theulaz, Irene, Epalinges, Switzerland  
 PA Kieta Holding SA, St-Prex, Switzerland (non-U.S. corporation)  
 PI US 6060241 20000509  
 AI US 1997-834776 19970403 (8)  
 PRAI US 1996-14906P 19960405 (60)

DT Utility  
FS Granted  
LN.CNT 2585  
INCL INCLM: 435/006.000  
INCLS: 536/023.200  
NCL NCLM: 435/006.000  
NCLS: 536/023.200  
IC [7]  
ICM C12Q001-70  
IPCI C12Q0001-70 [ICM,7]  
IPCR A61K0038-00 [N,A]; A61K0038-00 [N,C\*]; C12N0009-00 [I,A];  
C12N0009-00 [I,C\*]; C12N0009-10 [I,A]; C12N0009-10 [I,C\*];  
C12Q0001-68 [I,A]; C12Q0001-68 [I,C\*]  
EXF 536/23.2; 435/6  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 29 USPATFULL on STN  
AN 1999:85216 USPATFULL  
TI Compositions comprising isolated Helicobacter pylori CagI  
polynucleotides and method of preparation thereof  
IN Covacci, Antonello, Siena, Italy  
PA Chiron S.p.A., Italy (non-U.S. corporation)  
PI US 5928865 19990727  
AI US 1995-477451 19950607 (8)  
RLI Continuation-in-part of Ser. No. US 1995-425194, filed on 20 Apr 1995,  
now abandoned And Ser. No. US 1995-471491, filed on 6 Jun 1995 which is  
a division of Ser. No. US 256848  
PRAI IT 1992-FI52 19920302  
DT Utility  
FS Granted  
LN.CNT 6155  
INCL INCLM: 435/006.000  
INCLS: 435/007.320; 536/023.100  
NCL NCLM: 435/006.000  
NCLS: 435/007.320; 536/023.100  
IC [6]  
ICM C12Q001-68  
IPCI C12Q0001-68 [ICM,6]  
IPCR A61K0038-00 [N,C\*]; A61K0038-00 [N,A]; A61K0039-00 [N,C\*];  
A61K0039-00 [N,A]; C07K0014-195 [I,C\*]; C07K0014-205 [I,A];  
C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]  
EXF 435/7.32; 435/6; 536/23.1  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 29 USPATFULL on STN  
AN 1998:150478 USPATFULL  
TI Immunogenic compositions against helicobacter infection, polypeptides  
for use in the compositions, and nucleic acid sequences encoding said  
polypeptides  
IN Labigne, Agnes, Bures S/Yvette, France  
Suerbaum, Sebastin, Bochum, Germany, Federal Republic of  
Ferrero, Richard L., Paris, France  
Thiberge, Jean-Michel, Plaisir, France  
PA Institut Pasteur, Paris, France (non-U.S. corporation)  
Institut National de la Sante et de la Recherche Medicale, Paris, France  
(non-U.S. corporation)  
PI US 5843460 19981201  
AI US 1995-467822 19950606 (8)  
RLI Continuation of Ser. No. US 1995-447177, filed on 19 May 1995 which is a  
continuation-in-part of Ser. No. US 1995-432697, filed on 2 May 1995  
PRAI EP 1993-401309 19930519  
WO 1993-EP3259 19931119  
DT Utility  
FS Granted  
LN.CNT 3594

INCL INCLM: 424/234.100  
 INCLS: 435/007.320; 435/006.000; 435/007.900; 514/234.500; 514/041.000  
 NCL NCLM: 424/234.100  
 NCLS: 435/006.000; 435/007.320; 435/007.900; 514/041.000; 514/234.500  
 IC [6]  
 ICM A61K039-02  
 IPCI A61K0039-02 [ICM,6]  
 IPCR A61K0039-00 [N,C\*]; A61K0039-00 [N,A]; C07K0014-195 [I,C\*];  
 C07K0014-205 [I,A]; C07K0016-12 [I,C\*]; C07K0016-12 [I,A];  
 C12N0009-78 [I,C\*]; C12N0009-80 [I,A]; C12Q0001-68 [I,C\*];  
 C12Q0001-68 [I,A]  
 EXF 435/7.32; 435/4; 435/6; 435/7.9; 514/234.5; 514/41; 424/234.1  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AM286280 GenBank (R)  
 GenBank ACC. NO. (GBN): AM286280  
 GenBank VERSION (VER): AM286280.1 GI:110319990  
 SEQUENCE LENGTH (SQL): 1892616  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 12 Jul 2006  
 DEFINITION (DEF): Francisella tularensis subsp. tularensis strain FSC 198  
 complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: Francisella tularensis subsp. tularensis FSC 198  
 ORGANISM (ORGN): Francisella tularensis subsp. tularensis FSC 198  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Thiotrichales; Francisellaceae; Francisella  
 REFERENCE: 1  
 AUTHOR (AU): Chaudhuri, R.R.; Ren, C.P.; Desmond, L.; Vincent, G.A.;  
 Silman, N.J.; Brehm, J.; Elmore, M.J.; Hudson, M.J.;  
 Forsman, M.; Isherwood, K.E.; Gurycova, D.; Minton, N.P.;  
 Titball, R.W.; Pallen, M.J.; Vipond, R.  
 TITLE (TI): The complete genome sequence of the European  
 Francisella tularensis subspecies tularensis isolate  
 FSC 198 suggests that it is derived from the archetypal  
 laboratory strain Schu S4, originally isolated in North  
 America  
 JOURNAL (SO): Unpublished  
 REFERENCE: 2 (bases 1 to 1892616)  
 AUTHOR (AU): Chaudhuri, R.R.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (04-JUL-2006) Chaudhuri R.R., Division of  
 Immunity and Infection, University of Birmingham,  
 Vincent Drive, Edgbaston, Birmingham, B15 2TT, UNITED  
 KINGDOM

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1892616	/organism="Francisella tularensis subsp. tularensis FSC 198" /mol-type="genomic DNA" /strain="FSC 198" /sub-species="tularensis" /db-xref="taxon:393115" /country="Slovakia"

L7 ANSWER 13 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AM260522 GenBank (R)  
 GenBank ACC. NO. (GBN): AM260522



GenBank VERSION (VER): AM260522.1 GI:109713861  
 CAS REGISTRY NO. (RN): 899490-11-0  
 SEQUENCE LENGTH (SQL): 1553927  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 14 Nov 2006  
 DEFINITION (DEF): *Helicobacter acinonychis* str. Sheeba complete genome,  
 strain Sheeba.  
 KEYWORDS (ST): complete genome  
 SOURCE: *Helicobacter acinonychis* str. Sheeba  
 ORGANISM (ORGN): *Helicobacter acinonychis* str. Sheeba  
 Bacteria; Proteobacteria; Epsilonproteobacteria;  
 Campylobacteriales; Helicobacteraceae; Helicobacter  
 COMMENT:  
 Clone requests: scs@bx.psu.edu.  
 REFERENCE: 1  
 AUTHOR (AU): Eppinger, M.; Baar, C.; Linz, B.; Raddatz, G.; Lanz, C.;  
 Keller, H.; Morelli, G.; Gressmann, H.; Achtman, M.;  
 Schuster, S.C.  
 TITLE (TI): Who ate whom? Adaptive *Helicobacter* genomic changes  
 that accompanied a host jump from early humans to large  
 felines  
 JOURNAL (SO): PLoS Genet., 2 (7), E120 (2006)  
 REFERENCE: 2 (bases 1 to 1553927)  
 AUTHOR (AU): Schuster, S.C.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (27-MAR-2006) Schuster S.C., Department of  
 Biochemistry and Molecular Biology, Center for  
 Comparative Genomics and Bioinformatics Center for  
 Infectious Disease Dynamics, 310 Wartik Building, Penn  
 State University, University Park, PA 16802, USA Phone  
 +1 814 863-9278, FAX +1 814 863-6699

FEATURES (FEAT):  

Feature Key	Location	Qualifier
source	1..1553927	/organism="Helicobacter acinonychis str. Sheeba" /mol-type="genomic DNA" /strain="Sheeba" /db-xref="taxon:382638"

L7 ANSWER 14 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): CR626927 GenBank (R)  
 GenBank ACC. NO. (GBN): CR626927  
 GenBank VERSION (VER): CR626927.1 GI:60491031  
 CAS REGISTRY NO. (RN): 843924-26-5  
 SEQUENCE LENGTH (SQL): 5205140  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 17 Apr 2005  
 DEFINITION (DEF): *Bacteroides fragilis* NCTC 9343, complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: *Bacteroides fragilis* NCTC 9343  
 ORGANISM (ORGN): *Bacteroides fragilis* NCTC 9343  
 Bacteria; Bacteroidetes; Bacteroides (class);  
 Bacteroidales; Bacteroidaceae; Bacteroides  
 REFERENCE: 1 (bases 1 to 5205140)  
 AUTHOR (AU): Cerdeno-Tarraga, A.M.; Patrick, S.; Crossman, L.C.;  
 Blakely, G.; Abratt, V.; Lennard, N.; Poxton, I.;  
 Duerden, B.; Harris, B.; Quail, M.A.; Barron, A.; Clark, L.;  
 Corton, C.; Doggett, J.; Holden, M.T.; Larke, N.; Line, A.;  
 Lord, A.; Norbertczak, H.; Ormond, D.; Price, C.;

TITLE (TI): Rabbinoiwitsch,E.; Woodward,J.; Barrell,B.; Parkhill,J.  
 Extensive DNA inversions in the B. fragilis genome  
 control variable gene expression  
 JOURNAL (SO): Science, 307 (5714), 1463-1465 (2005)  
 OTHER SOURCE (OS): CA 142:234199  
 REFERENCE: 2 (bases 1 to 5205140)  
 AUTHOR (AU): Cerdeno-Tarraga,A.M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (29-JUL-2004) Cerdeno-Tarraga A.M., submitted  
 on behalf of the Pathogen Sequencing Unit, Sanger  
 Institute, Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA E-mail: amct@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..5205140	/organism="Bacteroides fragilis NCTC 9343" /mol-type="genomic DNA" /strain="ATCC 25285 = NCTC 9343" /db-xref="taxon:272559"

L7 ANSWER 15 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AE004969 GenBank (R)  
 GenBank ACC. NO. (GBN): AE004969  
 GenBank VERSION (VER): AE004969.1 GI:59717368  
 CAS REGISTRY NO. (RN): 432023-66-0  
 SEQUENCE LENGTH (SQL): 2153922  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 14 Feb 2005  
 DEFINITION (DEF): Neisseria gonorrhoeae FA 1090, complete genome.  
 SOURCE: Neisseria gonorrhoeae FA 1090  
 ORGANISM (ORGN): Neisseria gonorrhoeae FA 1090  
 Bacteria; Proteobacteria; Betaproteobacteria;  
 Neisseriales; Neisseriaceae; Neisseria  
 REFERENCE: 1 (bases 1 to 2153922)  
 AUTHOR (AU): Lewis,L.A.; Gillaspay,A.F.; McLaughlin,R.E.; Gipson,M.;  
 Ducey,T.F.; Ownbey,T.; Hartman,K.; Nydick,C.;  
 Carson,M.B.; Vaughn,J.; Thomson,C.; Song,L.; Lin,S.;  
 Yuan,X.; Najjar,F.; Zhan,M.; Ren,Q.; Zhu,H.; Qi,S.;  
 Kenton,S.M.; Lai,H.; White,J.D.; Clifton,S.; Roe,B.A.;  
 Dyer,D.W.  
 TITLE (TI): The Complete Genome Sequence of Neisseria gonorrhoeae  
 JOURNAL (SO): Unpublished  
 REFERENCE: 2 (bases 1 to 2153922)  
 AUTHOR (AU): Lewis,L.A.; Gillaspay,A.F.; McLaughlin,R.E.; Gipson,M.;  
 Ducey,T.F.; Ownbey,T.; Hartman,K.; Nydick,C.;  
 Carson,M.B.; Vaughn,J.; Thomson,C.; Song,L.; Lin,S.;  
 Yuan,X.; Najjar,F.; Zhan,M.; Ren,Q.; Zhu,H.; Qi,S.;  
 Kenton,S.M.; Lai,H.; White,J.D.; Clifton,S.; Roe,B.A.;  
 Dyer,D.W.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (10-MAR-2003) Microbiology and Immunology,  
 University of Oklahoma Health Sciences Center, 975 NE  
 10th St., Oklahoma City, OK 73104, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2153922	/organism="Neisseria gonorrhoeae FA 1090" /mol-type="genomic DNA"

/strain="FA 1090"  
/db-xref="taxon:242231"

L7 ANSWER 16 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AJ749949 GenBank (R)  
GenBank ACC. NO. (GBN): AJ749949  
GenBank VERSION (VER): AJ749949.1 GI:56603679  
CAS REGISTRY NO. (RN): 799222-54-1  
SEQUENCE LENGTH (SQL): 1892819  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 1 Mar 2006  
DEFINITION (DEF): Francisella tularensis subsp. tularensis SCHU S4  
complete genome.  
KEYWORDS (ST): complete genome  
SOURCE: Francisella tularensis subsp. tularensis SCHU S4  
ORGANISM (ORGN): Francisella tularensis subsp. tularensis SCHU S4  
Bacteria; Proteobacteria; Gammaproteobacteria;  
Thiotrichales; Francisellaceae; Francisella  
REFERENCE: 1  
AUTHOR (AU): Larsson, P.; Oyston, P.C.; Chain, P.; Chu, M.C.;  
Duffield, M.; Fuxelius, H.H.; Garcia, E.; Halltorp, G.;  
Johansson, D.; Isherwood, K.E.; Karp, P.D.; Larsson, E.;  
Liu, Y.; Michell, S.; Prior, J.; Prior, R.; Malfatti, S.;  
Sjostedt, A.; Svensson, K.; Thompson, N.; Vergez, L.;  
Wagg, J.K.; Wren, B.W.; Lindler, L.E.; Andersson, S.G.;  
Forsman, M.; Titball, R.W.  
TITLE (TI): The complete genome sequence of Francisella tularensis,  
the causative agent of tularemia  
JOURNAL (SO): Nat. Genet., 37 (2), 153-159 (2005)  
REFERENCE: 2 (bases 1 to 1892819)  
AUTHOR (AU): Duffield, M.L.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (25-JUN-2004) Duffield M.L., Biomedical  
Sciences, Defence Science and Technology Lab, Porton  
Down, Wiltshire, SP4 0JQ, UNITED KINGDOM

FEATURES (FEAT):  
Feature Key Location Qualifier  
=====+=====+=====

source	1..1892819	/organism="Francisella tularensis subsp. tularensis SCHU S4" /mol-type="genomic DNA" /strain="SCHU S4" /sub-species="tularensis" /db-xref="taxon:177416"
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L7 ANSWER 17 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AE014133 GenBank (R)  
GenBank ACC. NO. (GBN): AE014133 AE014853-AE015037  
GenBank VERSION (VER): AE014133.1 GI:24378526  
SEQUENCE LENGTH (SQL): 2030921  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 24 Jan 2006  
DEFINITION (DEF): Streptococcus mutans UA159, complete genome.  
SOURCE: Streptococcus mutans UA159  
ORGANISM (ORGN): Streptococcus mutans UA159  
Bacteria; Firmicutes; Lactobacillales;  
Streptococcaceae; Streptococcus  
COMMENT:

On or before Jan 18, 2006 this sequence version replaced

gi:24376380, gi:24376394, gi:24376399, gi:24376411, gi:24376427,  
gi:24376440, gi:24376449, gi:24376457, gi:24376467, gi:24376477,  
gi:24376489, gi:24376500, gi:24376508, gi:24376518, gi:24376529,  
gi:24376540, gi:24376558, gi:24376568, gi:24376580, gi:24376598,  
gi:24376611, gi:24376622, gi:24376632, gi:24376644, gi:24376656,  
gi:24376666, gi:24376676, gi:24376687, gi:24376701, gi:24376713,  
gi:24376731, gi:24376740, gi:24376746, gi:24376759, gi:24376773,  
gi:24376784, gi:24376798, gi:24376811, gi:24376821, gi:24376833,  
gi:24376843, gi:24376851, gi:24376864, gi:24376874, gi:24376885,  
gi:24376898, gi:24376914, gi:24376926, gi:24376935, gi:24376948,  
gi:24376961, gi:24376975, gi:24376986, gi:24376994, gi:24377004,  
gi:24377016, gi:24377027, gi:24377040, gi:24377051, gi:24377061,  
gi:24377070, gi:24377086, gi:24377096, gi:24377109, gi:24377120,  
gi:24377134, gi:24377145, gi:24377156, gi:24377170, gi:24377181,  
gi:24377193, gi:24377198, gi:24377208, gi:24377217, gi:24377232,  
gi:24377241, gi:24377253, gi:24377262, gi:24377272, gi:24377283,  
gi:24377293, gi:24377304, gi:24377317, gi:24377330, gi:24377345,  
gi:24377356, gi:24377366, gi:24377378, gi:24377385, gi:24377400,  
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gi:24378472, gi:24378487, gi:24378500, gi:24378511, gi:24378520.

REFERENCE: 1 (bases 1 to 2030921)  
AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;  
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;  
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;  
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.  
TITLE (TI): Genome sequence of Streptococcus mutans UA159, a  
cariogenic dental pathogen  
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439  
(2002)  
OTHER SOURCE (OS): CA 137:364100  
REFERENCE: 2 (bases 1 to 2030921)  
AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;  
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;  
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;  
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (09-JUL-2002) Department of Microbiology and  
Immunology, University of Oklahoma Health Sciences  
Center, 940 SL Young Blvd., Oklahoma City, OK 73104,  
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2030921	/organism="Streptococcus mutans UA159" /mol-type="genomic DNA"

/strain="UA159"  
/db-xref="taxon:210007"

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LOCUS (LOC): AE009952 GenBank (R)  
GenBank ACC. NO. (GBN): AE009952 AE013601-AE014015  
GenBank VERSION (VER): AE009952.1 GI:22002119  
SEQUENCE LENGTH (SQL): 4600755  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 2 May 2006  
DEFINITION (DEF): *Yersinia pestis* KIM, complete genome.  
SOURCE: *Yersinia pestis* KIM  
ORGANISM (ORGN): *Yersinia pestis* KIM  
Bacteria; Proteobacteria; Gammaproteobacteria;  
Enterobacteriales; Enterobacteriaceae; *Yersinia*

COMMENT:

On or before May 2, 2006 this sequence version replaced  
gi:21956656, gi:21956667, gi:21956674, gi:21956680, gi:21956691,  
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REFERENCE: 1 (bases 1 to 4600755)  
AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;  
Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;  
Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;  
Brubaker,R.R.; Plana,G.V.; Straley,S.C.;  
McDonough,K.A.; Nilles,M.L.; Matson,J.S.;  
Blattner,F.R.; Perry,R.D.  
TITLE (TI): Genome Sequence of *Yersinia pestis* KIM  
JOURNAL (SO): J. Bacteriol., 184 (16), 4601-4611 (2002)  
OTHER SOURCE (OS): CA 137:120475  
REFERENCE: 2 (bases 1 to 4600755)  
AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;  
Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;  
Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;  
Brubaker,R.R.; Plana,G.V.; Straley,S.C.;  
McDonough,K.A.; Nilles,M.L.; Matson,J.S.;  
Blattner,F.R.; Perry,R.D.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (21-FEB-2002) Genetics, University of  
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

# FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4600755	/organism="Yersinia pestis KIM" /mol-type="genomic DNA" /strain="KIM"

/db-xref="taxon:187410"

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LOCUS (LOC): AL111168 GenBank (R)  
GenBank ACC. NO. (GBN): AL111168 AL139074 AL139075 AL139076 AL139077 AL139078  
AL139079  
GenBank VERSION (VER): AL111168.1 GI:30407139  
SEQUENCE LENGTH (SQL): 1641481  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 14 Aug 2006  
DEFINITION (DEF): Campylobacter jejuni subsp. jejuni NCTC 11168 complete  
genome.  
KEYWORDS (ST): complete genome  
SOURCE: Campylobacter jejuni subsp. jejuni NCTC 11168  
ORGANISM (ORGN): Campylobacter jejuni subsp. jejuni NCTC 11168  
Bacteria; Proteobacteria; Epsilonproteobacteria;  
Campylobacteriales; Campylobacteraceae; Campylobacter

COMMENT:

On or before Aug 15, 2006 this sequence version replaced  
gi:6967505, gi:6967817, gi:6968128, gi:6968444, gi:6968723,  
gi:6968971.

Notes:

Details of C. jejuni sequencing at the Sanger Centre are available  
on the World Wide Web.

(URL, [http://www.sanger.ac.uk/Projects/C\\_jejuni/](http://www.sanger.ac.uk/Projects/C_jejuni/)).

REFERENCE:

1

AUTHOR (AU): Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.;  
Churcher, C.; Basham, D.; Chillingworth, T.; Davies, R.M.;  
Feltwell, T.; Holroyd, S.; Jagels, K.; Karlyshev, A.V.;  
Moule, S.; Pallen, M.J.; Penn, C.W.; Quail, M.A.;  
Rajandream, M.A.; Rutherford, K.M.; van Vliet, A.H.;  
Whitehead, S.; Barrell, B.G.

TITLE (TI): The genome sequence of the food-borne pathogen  
Campylobacter jejuni reveals hypervariable sequences

JOURNAL (SO): Nature, 403 (6770), 665-668 (2000)

OTHER SOURCE (OS): CA 132:147491

REFERENCE:

2

AUTHOR (AU): Gundogdu, O.; Bentley, S.D.; Dorrell, N.; Wren, B.W.;  
Parkhill, J.

TITLE (TI): Re-annotation of Campylobacter jejuni NCTC11168

JOURNAL (SO): Unpublished

REFERENCE:

3 (bases 1 to 1641481)

AUTHOR (AU): Parkhill, J.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-FEB-2000) Submitted on behalf of the  
Campylobacter sequencing team, Sanger Centre, Wellcome  
Trust Genome Campus, Hinxton, Cambridge CB10 1SA  
E-mail: parkhill@sanger.ac.uk

REFERENCE:

4 (bases 1 to 1641481)

AUTHOR (AU): Gundogdu, O.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (07-AUG-2006) Submitted on behalf of the  
Campylobacter sequencing team, Sanger Centre, Wellcome  
Trust Genome Campus, Hinxton, Cambridge CB10 1SA. In  
Collaboration with the Pathogen Molecular Biology  
Department at The London School of Hygiene & Tropical  
Medicine, London, Keppel Street, WC1E 7HT.  
E-mail: ozan.gundogdu@lshtm.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
-------------	----------	-----------

=====+=====+=====

source 1..1641481 /organism="Campylobacter jejuni  
subsp. jejuni NCTC 11168"  
/mol-type="genomic DNA"  
/strain="NCTC 11168"  
/sub-species="jejuni"  
/db-xref="taxon:192222"

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LOCUS (LOC): BA000007 GenBank (R)  
GenBank ACC. NO. (GBN): BA000007 AP002550-AP002569  
GenBank VERSION (VER): BA000007.2 GI:47118301  
CAS REGISTRY NO. (RN): 776960-28-2  
SEQUENCE LENGTH (SQL): 5498450  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 10 Apr 2007  
DEFINITION (DEF): Escherichia coli O157:H7 str. Sakai DNA, complete  
genome.  
SOURCE: Escherichia coli O157:H7 str. Sakai  
ORGANISM (ORGN): Escherichia coli O157:H7 str. Sakai  
Bacteria; Proteobacteria; Gammaproteobacteria;  
Enterobacteriales; Enterobacteriaceae; Escherichia

COMMENT:

On or before Nov 5, 2004 this sequence version replaced  
gi:13359456, gi:13359705, gi:13359995, gi:13360211, gi:13360491,  
gi:13360886, gi:13361156, gi:13361466, gi:13361764, gi:13362012,  
gi:13362333, gi:13362592, gi:13362858, gi:13363121, gi:13363382,  
gi:13363693, gi:13363930, gi:13364198, gi:13364484, gi:13364704.  
genome project

This work was done in collaboration with Tetsuya Hayashi, Makoto  
Ohnishi, Keisuke Nakayama (Miyazaki Medical College), Kozo Makino,  
Ken Kurokawa, Katsushi Yokoyama, Masashi Tanaka, Takeshi Honda,  
Teruo Yasunaga, Hideo Shinagawa (Osaka University), Takahiro Murata  
(Shinshu University), Chang-Gyun Han, Eiichi Ohtsubo, Toru Tobe,  
Chihiro Sasakawa (University of Tokyo), Hideto Takami (Japan Marine  
Science and Technology Center), Naotake Ogasawara (Nara Institute  
of Science and Technology), Satoru Kuhara (Kyuushu University), and  
supported by the Research for the Future Program of the Japan  
Society for the Promotion of Science.

REFERENCE:

1  
AUTHOR (AU): Makino, K.; Yokoyama, K.; Kubota, Y.; Yutsudo, C.H.;  
Kimura, S.; Kurokawa, K.; Ishii, K.; Hattori, M.;  
Tatsuno, I.; Abe, H.; Iida, T.; Yamamoto, K.; Onishi, M.;  
Hayashi, T.; Yasunaga, T.; Honda, T.; Sasakawa, C.;  
Shinagawa, H.  
TITLE (TI): Complete nucleotide sequence of the prophage VT2-Sakai  
carrying the verotoxin 2 genes of the enterohemorrhagic  
Escherichia coli O157:H7 derived from the Sakai  
outbreak

JOURNAL (SO): Genes Genet. Syst., 74 (5), 227-239 (1999)  
OTHER SOURCE (OS): CA 134:37762

REFERENCE:

2  
AUTHOR (AU): Ohnishi, M.; Murata, T.; Nakayama, K.; Kuhara, S.;  
Hattori, M.; Kurokawa, K.; Yasunaga, T.; Yokoyama, K.;  
Makino, K.; Shinagawa, H.; Hayashi, T.  
TITLE (TI): Comparative analysis of the whole set of rRNA operons  
between an enterohemorrhagic Escherichia coli O157:H7  
Sakai strain and an Escherichia coli K-12 strain MG1655  
JOURNAL (SO): Syst. Appl. Microbiol., 23 (3), 315-324 (2000)  
OTHER SOURCE (OS): CA 134:263368

REFERENCE:

3  
AUTHOR (AU): Yokoyama, K.; Makino, K.; Kubota, Y.; Watanabe, M.;  
Kimura, S.; Yutsudo, C.H.; Kurokawa, K.; Ishii, K.;



Hattori,M.; Tatsuno,I.; Abe,H.; Yoh,M.; Iida,T.;  
Ohnishi,M.; Hayashi,T.; Yasunaga,T.; Honda,T.;  
Sasakawa,C.; Shinagawa,H.

TITLE (TI): Complete nucleotide sequence of the prophage VT1-Sakai  
carrying the Shiga toxin 1 genes of the  
enterohemorrhagic Escherichia coli O157:H7 strain  
derived from the Sakai outbreak

JOURNAL (SO): Gene, 258 (1-2), 127-139 (2000)

OTHER SOURCE (OS): CA 135:71886

REFERENCE: 4

AUTHOR (AU): Hayashi,T.; Makino,K.; Ohnishi,M.; Kurokawa,K.;  
Ishii,K.; Yokoyama,K.; Han,C.G.; Ohtsubo,E.;  
Nakayama,K.; Murata,T.; Tanaka,M.; Tobe,T.; Iida,T.;  
Takami,H.; Honda,T.; Sasakawa,C.; Ogasawara,N.;  
Yasunaga,T.; Kuhara,S.; Shiba,T.; Hattori,M.;  
Shinagawa,H.

TITLE (TI): Complete genome sequence of enterohemorrhagic  
Escherichia coli O157:H7 and genomic comparison with a  
laboratory strain K-12

JOURNAL (SO): DNA Res., 8 (1), 11-22 (2001)

OTHER SOURCE (OS): CA 134:217892

REFERENCE: 5 (bases 1 to 5498450)

AUTHOR (AU): Hattori,M.; Ishii,K.; Shiba,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (26-JUN-2000) Masahira Hattori, Graduate  
School of Frontier Sciences, University of Tokyo; 5-1-5  
Kashiwanoha, Kashiwa, Chiba 277-8561, Japan  
(E-mail:hattori@k.u-tokyo.ac.jp, Tel:81-4-7136-4070,  
Fax:81-4-7136-4084)

# FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..5498450	/organism="Escherichia coli O157:H7 str. Sakai" /mol-type="genomic DNA" /strain="Sakai" /sub-strain="RIMD 0509952" /serovar="O157:H7" /db-xref="taxon:386585"

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LOCUS (LOC): BX571965 GenBank (R)

GenBank ACC. NO. (GBN): BX571965

GenBank VERSION (VER): BX571965.1 GI:52208053

CAS REGISTRY NO. (RN): 755924-52-8

SEQUENCE LENGTH (SQL): 4074542

MOLECULE TYPE (CI): DNA; circular

DIVISION CODE (CI): Bacteria

DATE (DATE): 17 Apr 2005

DEFINITION (DEF): Burkholderia pseudomallei strain K96243, chromosome 1,  
complete sequence.

SOURCE: Burkholderia pseudomallei K96243

ORGANISM (ORGN): Burkholderia pseudomallei K96243  
Bacteria; Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia;  
pseudomallei group

REFERENCE: 1 (bases 1 to 4074542)

AUTHOR (AU): Holden,M.T.; Titball,R.W.; Peacock,S.J.;  
Cerdeno-Tarraga,A.M.; Atkins,T.; Crossman,L.C.;  
Pitt,T.; Churcher,C.; Mungall,K.; Bentley,S.D.;  
Sebahia,M.; Thomson,N.R.; Bason,N.; Beacham,I.R.;  
Brooks,K.; Brown,K.A.; Brown,N.F.; Challis,G.L.;

Cherevach, I.; Chillingworth, T.; Cronin, A.; Crossett, B.; Davis, P.; DeShazer, D.; Feltwell, T.; Fraser, A.; Hance, Z.; Hauser, H.; Holroyd, S.; Jagels, K.; Keith, K.E.; Maddison, M.; Moule, S.; Price, C.; Quail, M.A.; Rabinowitsch, E.; Rutherford, K.; Sanders, M.; Simmonds, M.; Songsivilai, S.; Stevens, K.; Tumapa, S.; Vesaratchavest, M.; Whitehead, S.; Yeats, C.; Barrell, B.G.; Oyston, P.C.; Parkhill, J.

TITLE (TI): Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (39), 14240-14245 (2004)

OTHER SOURCE (OS): CA 141:289864

REFERENCE: 2 (bases 1 to 4074542)

AUTHOR (AU): Holden, M.T.G.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (01-SEP-2004) Submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: mh3@sanger.ac.uk

# FEATURES (FEAT):

Feature Key	Location	Qualifier
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L7 ANSWER 22 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): BX936398 GenBank (R)

GenBank ACC. NO. (GBN): BX936398

GenBank VERSION (VER): BX936398.1 GI:51587641

CAS REGISTRY NO. (RN): 736028-02-7

SEQUENCE LENGTH (SQL): 4744671

MOLECULE TYPE (CI): DNA; circular

DIVISION CODE (CI): Bacteria

DATE (DATE): 17 Apr 2005

DEFINITION (DEF): *Yersinia pseudotuberculosis* IP32953 genome, complete sequence.

KEYWORDS (ST): complete genome

SOURCE: *Yersinia pseudotuberculosis* IP 32953

ORGANISM (ORGN): *Yersinia pseudotuberculosis* IP 32953  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Yersinia*

REFERENCE: 1 (bases 1 to 4744671)

AUTHOR (AU): Chain, P.S.; Carniel, E.; Larimer, F.W.; Lamerdin, J.; Stoutland, P.O.; Regala, W.M.; Georgescu, A.M.; Vergez, L.M.; Land, M.L.; Motin, V.L.; Brubaker, R.R.; Fowler, J.; Hinnebusch, J.; Marceau, M.; Medigue, C.; Simonet, M.; Chenal-Francisque, V.; Souza, B.; Dacheux, D.; Elliott, J.M.; Derbise, A.; Hauser, L.J.; Garcia, E.

TITLE (TI): Insights into the evolution of *Yersinia pestis* through whole-genome comparison with *Yersinia pseudotuberculosis*

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (38), 13826-13831 (2004)

OTHER SOURCE (OS): CA 141:272420

REFERENCE: 2 (bases 1 to 4744671)

AUTHOR (AU): Chain, P.S.G.; Carniel, E.; Garcia, E.; Larimer, F.W.

TITLE (TI): Direct Submission

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185511..186149

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aldolase from Escherichia coli  
(213 aa) fasta scores; E(): 0,  
55.7% identity in 203 aa overlap.  
Contains Pfam match to entry  
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AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007  
SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

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31  FILE ADISCTI  
10  FILE ADISINSIGHT  
27  FILE ADISNEWS  
3911 FILE AGRICOLA  
116  FILE ANABSTR  
16  FILE ANTE  
41  FILE AQUALINE  
1216 FILE AQUASCI  
3267 FILE BIOENG  
30282 FILE BIOSIS  
10641 FILE BIOTECHABS  
10641 FILE BIOTECHDS  
19601 FILE BIOTECHNO  
10704 FILE CABA  
37645 FILE CAPLUS  
790  FILE CEABA-VTB  
81  FILE CIN  
319  FILE CONFSCI  
4  FILE CROPB  
133  FILE CROPU  
29  FILE DDFB  
170  FILE DDFU  
38469 FILE DGENE  
2384  FILE DISSABS  
29  FILE DRUGB  
566  FILE DRUGU  
125  FILE EMBAL  
21269 FILE EMBASE  
10560 FILE ESBIODASE  
16  FILE FOREGE  
411  FILE FROSTI  
1211 FILE FSTA  
515097 FILE GENBANK  
61  FILE HEALSAFE  
6488 FILE IFIPAT
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12 FILE IMSDRUGNEWS  
 9 FILE IMSRESEARCH  
 25 FILE KOSMET  
 17980 FILE LIFESCI  
 39232 FILE MEDLINE  
 240 FILE NTIS  
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 371 FILE OCEAN  
 13245 FILE PASCAL  
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 84 FILE PHIN  
 745 FILE PROMT  
 3 FILE PROUSDDR  
 3 FILE RDISCLOSURE  
 19895 FILE SCISEARCH  
 9853 FILE TOXCENTER  
 65679 FILE USPATFULL  
 7383 FILE USPAT2  
 1 FILE VETB  
 161 FILE VETU  
 68 FILE WATER  
 8559 FILE WPIDS  
 31 FILE WPIFV  
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 42 FILE IPA  
 4 FILE NAPRALERT  
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 L3 739 SEA L2(S) PYLORI?  
 L4 49 SEA L3 AND (BCC? OR ?CCATC?)  
 L5 47 DUP REM L4 (2 DUPLICATES REMOVED)  
 D TI L5 1-45  
 D TI L5 46-47  
 L6 31 SEA L3 AND (BCC? OR CCATC?)  
 L7 29 DUP REM L6 (2 DUPLICATES REMOVED)  
 D L7 1-29

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FILE GENBANK

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This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE USPATFULL

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 10 Apr 2007 (20070410/PD)

FILE LAST UPDATED: 10 Apr 2007 (20070410/ED)

HIGHEST GRANTED PATENT NUMBER: US7203969

HIGHEST APPLICATION PUBLICATION NUMBER: US2007079413

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REVISED CLASS FIELDS (/NCL) LAST RELOADED: Oct 2006